



**FIGURE 1a**  
**(SEQ ID NO: 1 and SEQ ID NO: 2)**

TTTAATCATG GAATATTCTA AACATACAGA AAAATCACAG AAAATAATA ACAACCCACTC ATTATATCTTC  
TCCCCAACCC CATGTAATAA ATATTTAAAT ATTCGTGTTAA ATGCTAAATT TAACACATGC TAAACGTTCC  
TOCCTGGATG TGGTGGCTCA CCCCTGTAAT CCCAGTACTT TGGGAGGAGG AGCTGGGAGG ATTGCTTGAG  
TCCAGGAGCT CGACACCCAGC ATGGGAAACA TAGTGGCAGTC TCGCTCTCAC AAAAACAAA AAAATTAGCT  
GGGCATGGTG CTCTGCACTCA GAAATCCCAG TGACTGGGAG GCTGAGGTGG GAGAATTGCT TGACTCTGGG  
AATTTGAGGC TCCAGTGAGC CCTGATCATG CCACTGCACTT CCAGCATGG CGACATAGCA AAACTTGTC  
AAAAAAAAAA AAGTTTCTC TCTGGCCCCAC CATAGACAAAC CACTCTCTG ATTCTATATCT TCCTAGATGA

-1101  
-1031  
-961  
-891  
-821  
-751  
-681

API

ATTTTGCCCA TTCTCTTCTA TATGAAAGGA ACCAGACATT AGCCATTCTG GTCTCTCGTT TCTTTCACCTT  
AAGATAAAAT TCACTTAACC TGTATTGTTG TACAGAACTG CAGTTCTTC TTTGTTATTT ATTGTAAGA  
CAGGGTCTGG CTATGTTGCC TAGGCTGCTC TCGAACGTGTG GGCCTCAAGC AATCACCTG CCAAGCTCTG  
GGACCCACAGG CATGACCCAT GGCACTCTAT CTGACTTTG ATCTTATTTT TTGCTGACTA CTAGCCCCATG

-511  
-561  
-471  
-401

CONTACT: METABOLIC SYSTEMS TECHNOLOGY INC., 10000 UNIVERSITY DRIVE, SUITE 100, BURBANK, CA 91504, USA

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CTAGCTCCCC TCTCTCTGCCTCTCTCCAG GCTCACATCC ACATGCCAAG ACCTCTGCAG CCATTCTGCT

-261

**8ts**  
TCCCTCTCTT CCACCTCTGT CCCACCTCAQ AGAGCTACGG GGCTCCCTGG CTACCAACTG GCTCCCTGAGG  
5p1 / 5p2  
5p1 / 5p3

- 191

CCTCCCCGAG GGTGGCTTC TGGGAGAAGG AAGCCAGGTC CCTGCAGGTT GTGGGACCCCC ACACAATGAG  
Sp1/Sp3 Sp1/Sp3  
Sp1/Sp3 ETS

- 121 -

GGTTTTCCCC CAGGATGTTG TGTCCCCCTG CCCCCACTTC TGTCCATAA TTAAACCACCC CCTCTCTTAC  
*Sp1/Sp3* +1  
 CACTGTGCCCTCTTCCTGAGG CCCCCATCA TTTTTAACTACCCCTCTG GAGGGTGTAGC

-51

Ets Ets  
ACCTTCTGTG CTCTGTCCCC AACCTTCCAC TTCCCCCTCAA CGCGCTGCTC AGGGATGACC TTGGGCACTG

90

M T P G T  
TGCCTTCTTCT GAGTGGtaag tggggccagg gtactgggg aagcttgg a gggatctcga ggggactcca  
V L L L S

160

tctggggaggc caggctgggg gctgggtggc ggctccaacc actcttatgca ggagctgagg cagggggagt  
 ctccatgtgc gagtgcccg gagtcagtag agtgtgaccc gaatgaagag gggctcaggc gctgtgtc  
 ggttgcgact aagctaccc tccagctggc tttgtgtcc caggcttcc tttctccact catggagtc  
 ctgtgtggg tgacagaggt cttcccaacc tccccccggg gtggaaaggcc acagaagccca ccaggggaggc  
 gggaaagggtg yacatcacct cctggggct nnnnnnnncc ccaagtcctg actgcacgta gggaaaggcc  
 INTRON 1

230  
300  
370  
440  
510

ccccctgtcgtaa aaactgcata agagtcacat tcacgtgcctc tcaaaaatca ggcttggctg ggtgcgggtgg  
 etcatgttta taatcccgac actttggag gccgagatgg gctgtatcccc tgaggtcagg agtttgcac  
 cagccctggcc aacatggta aaccccatct ttacccaaaaataaaaaattt agccgggcat ggtggcgatgc  
 acttgtaaatc cccgtctttt gggaaagctga ggcaagagaa tcgcttgaccc agccgggcat ggtggcgatgc  
 ttagctgaga tcgtggcggtt gcaatccggc ctcagcaaca gagegagact tcatctaaa aaaaaaaaaaaaaaaa  
 aaaaaaaaaaaa aaaaaagaaa aagaggtgg gagggtcttag ggatggggc tcttttaact cccagccctcc  
 tcgcggccacca aatatttcctc agTCTGGCT TCTTATCATG GATTCAACCT CGATCTCCAC GAGCCTACGA  
 V L A S Y H G F N L D V E E P T

580  
650  
720  
790  
860  
930  
1000



**FIGURE 1b**  
**(SEQ ID NO: 1 and SEQ ID NO: 2)**

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TCTTCCAGGA GGATGCAGGC CGCTTTGGC AGAGCGTGGT GCAGTTGGT GGATCTCC <u>gt</u> aggccccact	1070
I F Q E D A G G F G Q S V V Q F G G S R	
<u>INTRON 2 (3019 bp)</u>	
cccccaagtg cccgtgtctc ccacccctcc tgtggctgca gtgacatggc catgggtgtg <u>tccca</u> ACT	4080
L	
CGTGGTGGGA CCACCCCTCG ACCTCTCGC GCCCAACCAG ACGGCACCGC TCTATCACTC CGCAGCTGCC	4150
V V G A P L E V V A A N Q T G R L Y D C A A A	
ACCCCATGT CCCAGCCAT CCCGCTCCAC <u>Agt</u> agtgac cacctggaa ttggggccctt caacccctct	4220
T G M C Q P I P L H <u>INTRON 3</u>	
ggaccccaact gtggcccccgc ttatgttca gtccagaccc tccccggcaaa tgagtgtgtg ctgtgagtga	4290
gaccccccgt gtatgtccctt <u>gcag</u> TCCGCC CTCAGCCCT AACATGTCC TTGGGCTGA CCCTCCGAGC	4360
I R P E A V N M S L G L T L A A	
CTCCACCAAC GGCTCCCCGC TCCTGG <u>gt</u> agtgatcc ttggccacggg ggggtgggtt gggggggggg	4430
S T N G S R L L <u>INTRON 4</u>	
gttttgttgg ggaggaggtt ggggtttggga gtggaggagg agggtgtgtt agggactctt ggctcacagg	4500
cttctgtcc <u>cag</u> CCCTCTG GCCCCCACCT CCACAGAGTC TGTGGGAGCA ACTCATACTC AAAGGGTTCC	4570
A C G P T L H R V C G E N S Y S K G S	
TCCTCTCTGC TGCCCTCGC CTGGAGAGTC ATCCAGACAG TCCCCGACGC CACCCAC <u>gt</u> Aggtccctgg	4640
C L L L G S R W E I I Q T V P D A T P	
<u>INTRON 5 (4267 bp)</u>	
caggagctgc aggagggggtt tggggccccc <u>cagt</u> gtatctt cccattcccc <u>cacag</u> AGTGT	8840
E C	
CCACATCAAG AGATGGACAT CCTCTTCTG ATTGACGGCT CTGGAAGCAT TGACCAAAAT CACTTTAAC	8910
P H Q E M D I V F L I D G S G S I D Q N D F N	
AGATCAAGGC CTTTGTCCAA CCTGTCATGG GCCAGTTGA GGGCACTGAC ACCCTG <u>gt</u> ga agactgggca	8980
Q M K G F V Q A V M G Q F E G T D T L	
<u>INTRON 6 (1255 bp)</u>	
aacaatagta acaggcactg agccctggc ccccccaact ggcccttgc <u>a</u> TTGGCACTG ATGCAGTACT	10240
P A L M Q Y	
CAAACCTCT GAAGATCCAC TTCACCTCA CCCAATTCCG GACCAGCCCG AGCCAGGAGA CCCTGGTGGA	10310
S N L L K I H F T F T Q F R T S P S Q Q S L V D	
TCCCATGTC CAACTGAAAG CCCTGACGTT CACGGCCACG CCCATCTGA CAGTGGT <u>gt</u> ta aagcaacccc	10380
P I V Q L K G L T Y T A T G I L T V	
ccccca..... <u>INTRON 7</u>	



Replacement Sheet

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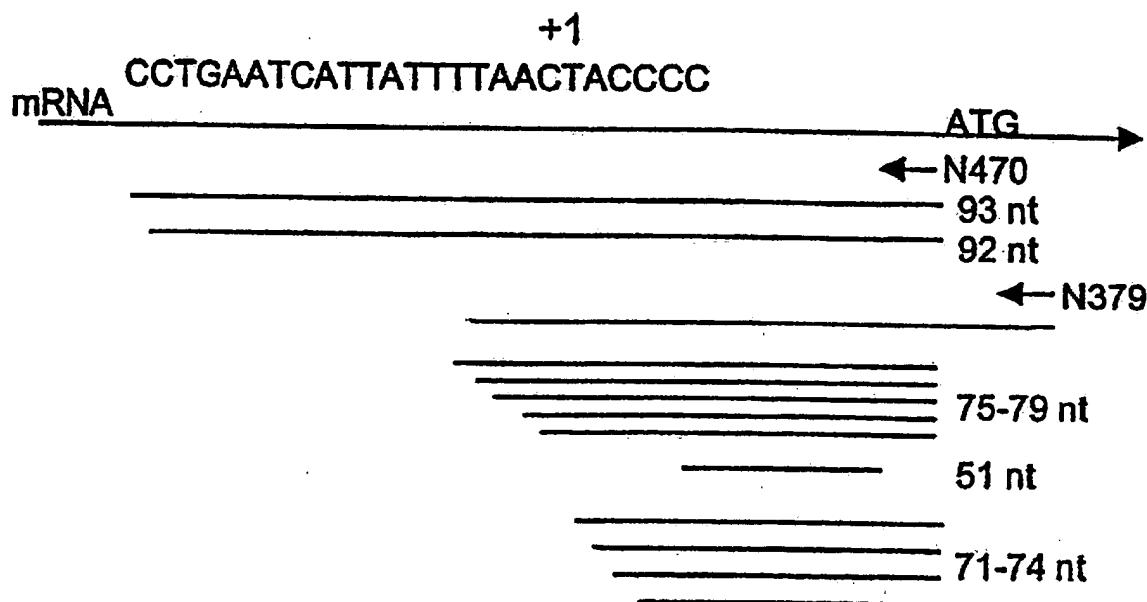
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FIGURE 3

SEQ ID NO: 4 (Also positions 1152 to 1176 of SEQ ID NO: 1)

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FIGURE 8

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SEQ ID NOS: 5 and 6

(SEQ ID NOS: 5 and 6 are collectively  
positions 1095 to 1140 of SEQ ID NO: 1)

1	2	3	4	5	6	7	8	9	10
-76				-66				-54	
CCATAATTAAACCA	C	G	C	C	C	C	T	C	C
●	○	○	○	○	○	○	○	○	○
-53					-38			-31	
ACCCACTGTGCCCCT	T	T	T	C	C	T	G	C	T
○	●	○	○	○	○	○	○	○	○

(SEQ ID NO: 5)

(SEQ ID NO: 6)



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Sequence Range: -11390 to 10387  
(SEQ ID NO:3)

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Translational stop codon for CDllc

FIGURE 9

Protein Sequence: SEQ ID NO:2

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-11321  
TGATCCCTCT TTGCCTTGGGA CTTCTTCTCC CGCGATTTTC CCCACTTACT TACCCCTCACC TGTCAGGCTG  
  
-11251  
ACGGGGAGGA ACCACTGCAC CACCGAGAGA GGCTGGGATG GGCTGCTTC CTGTCTTGG GAGAAAACGT  
  
-11181  
CTTGCTTGGG AAGGGGCCTT TGTCTTGTCA AGGTTCCAAC TGGAAACCCCT TAGGACAGGG TCCCTGCTGT  
  
-11111  
GTTCCCCAAA AGGACTTGAC TTCGAATTTTC TACCTAGAAA TACATGGACA ATACCCCCAG GCCTCAGTCT  
  
-11041  
CCCTTCTCCC ATGAGGCACG AATGATCTTT CTTTCTTTC CTTTTTTTTT TTTTCTTTT CTTTTTTTTT  
  
-10971  
TTTTTGAGA CGGAGTCTCG CTCTGTCACC CAGGCTGGAG TGCAATGGCG TGATCTCGGC TCGCTGCAAC  
  
-10901  
CTCCGCCCTCC CGGGTCAAG TAATTCTGCT GTCTCAGCCT CCTGCGTAGC TGGGACTACA GGCACACGCC  
  
-10831  
ACCTCGCCCCG GCCCGATCTT TCTAAAATAC AGTTCTGAAT ATGCTGCTCA TCCCCACCTG TCTTCAACAG  
  
-10761  
CTCCCCATTA CCCTCAGGAC AATGTCAGA CTCTCCAGCT TCGCGTGAGA AGTCCCCCTTC CATCCCCAGAG  
  
-10691  
GGTGGGCTTC AGGGCGCACA GCATGAGAGC CTCTGTGCC CCATCACCCCT CGTTCCAGT GAATTAGTGT  
  
-10621  
CATGTCAGCA TCAGCTCAGG CCTTCATCGT GGGGCTCTCA GTTCCGATTG CCCAGGCTGA ATTGGGAGTG  
  
-10551  
AGATGCCTGC ATGCTGGTT CTGCACAGCT GGCCTCCCGC GTTGGGTCA ACATTGCTGG CCTGGAAGGG  
  
-10481  
AGGAGCGCCC TCTAGGGAGG GACATGGCCC CGGTGCGGCT GCAGCTCACC AGCCCCAGGG GCAGAAAGAGA  
  
-10411  
CCCAACCAC TCCATTCTTG TGAGGCTATG AATATAGTAC CTGAAAAAAT GCCAAGCACT AGATTATTTT  
  
-10341  
TTTAAAAAGC GTACTTTAAA TGTTTGTGTT AATACACATT AAAACATGCA CAAAAGATG CATCTACCGC  
  
-10271  
TCTTGGAAA TATGTCAAAG GGTCTAAAAA TAAAAAAGCC TTCTGTGGAT ATGAGTCCTG AAGGATGACA  
  
-10201  
CCCATGGGGT CCCTTACCA CGGTGGACCC TGGCCAGCAC TGAGGCCTGG GGCCAGGACA AGAAGTTAAC  
  
-10131  
CAGAGTAGGG TTGTGAATAT CCCTCTCTTG GAAGTAACCT GACCTCTAA TCTGCTCACT CCACTCTCAG  
  
-10061